



## SEQUENCE LISTING

Anderson et al.

&lt;120&gt; CRYSTAL STRUCTURE OF GLUTAMATE RACEMASE (MURI)

&lt;130&gt; ASZD-P01-007

&lt;140&gt; 10/729,571

&lt;141&gt; 2003-12-05

&lt;150&gt; 60/435,272

&lt;151&gt; 2002-12-20

&lt;150&gt; 60/435,167

&lt;151&gt; 2002-12-20

&lt;150&gt; 60/435,087

&lt;151&gt; 2002-12-20

&lt;150&gt; 60/435,527

&lt;151&gt; 2002-12-20

&lt;160&gt; 76

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 768

&lt;212&gt; DNA

&lt;213&gt; H. pylori

&lt;221&gt; CDS

&lt;222&gt; (1)..(768)

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Lys	Ser	Leu	Leu	Lys	Ala	Arg	Leu	Phe	Asp	Glu	Ile	Ile	Tyr	Tyr	Gly	
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Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu	
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Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala		
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Phe	Val	Pro	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu		
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act	tgc	atg	cat	tat	tat	ttc	act	ccc	tta	gag	att	tta	ccc	gaa	gtg		528
Thr	Cys	Met	His	Tyr	Tyr	Phe	Thr	Pro	Leu	Glu	Ile	Leu	Pro	Glu	Val		
				165					170					175			
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Ile	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	Gln	Lys	Ile	Glu		
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His	Ser	Gly	Asp	Ala	Ile	Val	Glu	Tyr	Leu	Gln	Gln	Lys	Tyr	Ala	Leu		
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gat	gtg	atc	tgg	cta	gaa	aga	caa	gct	aaa	gaa	tgg	ctc	aaa	ttg	taa		768
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 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu  
 65 70 75 80  
 Met Gln Lys Tyr Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser  
 85 90 95  
 Ile Leu Ala Ile Lys Arg Gln Val Glu Asp Lys Asn Ala Pro Ile Leu  
 100 105 110  
 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala  
 115 120 125  
 Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu  
 130 135 140  
 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu  
 145 150 155 160  
 Thr Cys Met His Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val  
 165 170 175  
 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu  
 180 185 190  
 Gly Tyr Phe Met Gly His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile  
 195 200 205  
 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu  
 210 215 220  
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 225 230 235 240  
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<221> CDS  
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Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly	
20 25 30	
gat agc gct aga gtg cct tat ggc act aaa gac ccc act acg atc aag	144
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys	
35 40 45	
caa ttt ggc tta gag gct ttg gat ttt ttc aaa cca cac cag att gaa	192
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu	
50 55 60	
tta ttg att gtg gca tgc aac acc gca agc gct ctg gct tta gaa gag	240
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu	
65 70 75 80	
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85 90 95	
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gtg cta ggg aca aaa gcg acg att caa tcc aac gct tat gac aac gcc	384
Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala	
115 120 125	
ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt	432
Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu	
130 135 140	
ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gag	480
Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu	
145 150 155 160	
act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg	528
Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val	
165 170 175	
att att tta ggt tgc acg cat ttt ccc ttg att gct caa aaa att gag	576
Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu	
180 185 190	
ggc tat ttc atg gag cat ttt gcc ctt cca acg ccc ccc cta ctc atc	624

Gly Tyr Phe Met Glu His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile  
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 225 230 235 240  
 gat gtg atc tgg cta gaa aga caa gct aaa gaa tgg ctc aaa ttg taa 768  
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 85 90 95  
 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu  
 100 105 110  
 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala  
 115 120 125  
 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu  
 130 135 140

Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu  
145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val  
165 170 175

Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu  
180 185 190

Gly Tyr Phe Met Glu His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile  
195 200 205

His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu  
210 215 220

Lys Asn Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly  
225 230 235 240

Asp Val Ile Trp Leu Glu Arg Gln Ala Lys Glu Trp Leu Lys Leu  
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Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly	
20 25 30	
gat agc gct aga gtg cct tat ggc act aaa gac ccc act acg atc aag	144
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys	
35 40 45	
caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gaa	192
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu	
50 55 60	
tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag	240
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu	
65 70 75 80	

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 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser  
 85 90 95

att tta gcg atc aag cga caa gta aaa gat aaa aac gcc cct att tta 336  
 Ile Leu Ala Ile Lys Arg Gln Val Lys Asp Lys Asn Ala Pro Ile Leu  
 100 105 110

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 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala  
 115 120 125

ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt 432  
 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu  
 130 135 140

ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa 480  
 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu  
 145 150 155 160

act tgc atg cgt tat tat ttc act ccc tta aag att tta ccc gaa gtg 528  
 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val  
 165 170 175

att att tta ggt tgc acg cat ttt ccc tta atc gct caa aaa att gag 576  
 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu  
 180 185 190

ggc tat ttt atg gag cat ttt gcc ctt tca aca ccc ccc cta ctc atc 624  
 Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile  
 195 200 205

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 His Ser Gly Asp Ala Ile Val Gly Tyr Leu Gln Gln Lys Tyr Ala Leu  
 210 215 220

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 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly  
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gat gtg atc tgg cta gaa aaa caa gct aaa gaa tgg ctc aaa ttg taa 768  
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Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu  
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Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu  
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Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser  
           85                  90                  95

Ile Leu Ala Ile Lys Arg Gln Val Lys Asp Lys Asn Ala Pro Ile Leu  
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Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala  
       115                  120                  125

Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu  
   130                  135                  140

Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu  
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Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val  
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           180                  185                  190

Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile  
       195                  200                  205

His Ser Gly Asp Ala Ile Val Gly Tyr Leu Gln Gln Lys Tyr Ala Leu  
   210                  215                  220

Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly  
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Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly	
20 25 30	
gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag	144
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys	
35 40 45	
caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa	192
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys	
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Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu	
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atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc	288
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85 90 95	
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100 105 110	
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Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala	
115 120 125	
ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt	432
Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu	
130 135 140	
ttt gtg cct ttg att gaa gaa agt att tta ggg ggc gaa ttg tta gaa	480
Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Gly Gly Glu Leu Leu Glu	
145 150 155 160	
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Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val	
165 170 175	
att att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag	576
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 Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile  
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cat tcg ggc gat gct att gtg gaa tat ttg cag caa aaa tac gcc ctt 672  
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aag aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc 720  
 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly  
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gat gtg atc tgg cta gaa aaa cag gct aa 749  
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Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys  
 35 40 45

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys  
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Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu  
 65 70 75 80

Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser  
 85 90 95

Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu  
 100 105 110

Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala  
 115 120 125

Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu  
 130 135 140

Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Gly Gly Glu Leu Leu Glu  
145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val  
165 170 175

Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu  
180 185 190

Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile  
195 200 205

His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu  
210 215 220

Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly  
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20 25 30

gat agt gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag 144  
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys  
35 40 45

caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gga 192  
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly  
50 55 60

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                   130                                  135                                  140

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 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val  
                                   165                                  170                                  175

gtt att tta ggt tgc acg cat ttt ccc tta atc gct caa aaa att gag 576  
 Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu  
                   180                                  185                                  190

ggc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc cta ctc atc 624  
 Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile  
                   195                                  200                                  205

cat tcg ggc gat gct att gtg gaa tat ttg cag caa aaa tac gcc ctt 672  
 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu  
                   210                                  215                                  220

aaa aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agt ggc 720  
 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly  
                   225                                  230                                  235                                  240

gat gtg atc tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa 768  
 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu  
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Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly

20	25	30
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys		
35	40	45
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly		
50	55	60
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu		
65	70	75
Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser		
85	90	95
Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Ser Ile Leu		
100	105	110
Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala		
115	120	125
Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu		
130	135	140
Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu		
145	150	155
Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val		
165	170	175
Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu		
180	185	190
Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile		
195	200	205
His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu		
210	215	220
Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly		
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Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly	
20 25 30	
gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag	144
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys	
35 40 45	
caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa	192
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys	
50 55 60	
tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag	240
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu	
65 70 75 80	
atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc	288
Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser	
85 90 95	
att tta gcg atc aag caa caa gta aaa gat aaa aac gcc cct att tta	336
Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu	
100 105 110	
gtg cta ggg aca aaa gcg acg att caa tct aac gct tat gac aac gcc	384
Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala	
115 120 125	
cta aaa caa caa ggc tat ttg aac att tcg cat tta gcc act tct ctt	432
Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu	
130 135 140	
ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gag	480
Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu	
145 150 155 160	
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Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val	
165 170 175	
atc att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag	576
Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu	
180 185 190	

ggc tat ttt atg gag cat ttt gcc ctt cca acc ccc ccc cta ctc atc 624  
 Gly Tyr Phe Met Glu His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile  
 195 200 205

cat tcg ggc gat gct att gta gaa tat ttg cag caa aaa tac acc ctt 672  
 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Thr Leu  
 210 215 220

aag aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agt ggc 720  
 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly  
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Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys  
 35 40 45

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys  
 50 55 60

Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu  
 65 70 75 80

Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser  
 85 90 95

Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu  
 100 105 110

Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala  
 115 120 125

Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu

130                      135                      140  
 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu  
 145                      150                      155                      160  
 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val  
                     165                      170                      175  
 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu  
                     180                      185                      190  
 Gly Tyr Phe Met Glu His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile  
                     195                      200                      205  
 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Thr Leu  
                     210                      215                      220  
 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly  
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 1                      5                      10                      15  
 aaa agc ctt tta aaa gcg caa att ttt gat gaa atc atc tat tat ggc                      96  
 Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly  
                     20                      25                      30  
 gat agt gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag                      144  
 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys  
                     35                      40                      45  
 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gga                      192  
 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly  
                     50                      55                      60  
 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag                      240  
 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu



65	70	75	80	
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Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser				
	85	90	95	
att tta gcg atc aaa caa caa gtg aaa gat aaa aac gct cct att tta				336
Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu				
	100	105	110	
gtg cta ggg aca aaa gcg acg att caa tct aac gct tac gat aac gcc				384
Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala				
	115	120	125	
ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt				432
Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu				
	130	135	140	
ttt gtg cct ttg att gaa gaa aat att tta gag ggc gaa ttg cta gaa				480
Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu				
	145	150	155	160
act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg				528
Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val				
	165	170	175	
atc att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag				576
Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu				
	180	185	190	
ggc tat ttt atg gag cat ttt gcc ctt tta acg ccc ccc cta ctc atc				624
Gly Tyr Phe Met Glu His Phe Ala Leu Leu Thr Pro Pro Leu Leu Ile				
	195	200	205	
cat tct ggc gat gct att gta gaa tat ttg caa caa aaa tac gcc ctt				672
His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu				
	210	215	220	
aag aaa aat gca cac tca ttc cct aaa gtg gaa ttt cat gcg agc gcc				720
Lys Lys Asn Ala His Ser Phe Pro Lys Val Glu Phe His Ala Ser Gly				
	225	230	235	240
gat gtg atc tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa				768
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 20 25 30

Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys  
 35 40 45

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly  
 50 55 60

Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu  
 65 70 75 80

Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser  
 85 90 95

Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu  
 100 105 110

Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala  
 115 120 125

Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu  
 130 135 140

Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu  
 145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val  
 165 170 175

Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu  
 180 185 190

Gly Tyr Phe Met Glu His Phe Ala Leu Leu Thr Pro Pro Leu Leu Ile  
 195 200 205

His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu  
 210 215 220

Lys Lys Asn Ala His Ser Phe Pro Lys Val Glu Phe His Ala Ser Gly  
 225 230 235 240

Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu

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1 5 10 15				
aaa agc ctt tta aaa gcg caa att ttt gat gaa atc atc tat tat ggc				96
Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly				
20 25 30				
gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag				144
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys				
35 40 45				
caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gaa				192
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu				
50 55 60				
tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag				240
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu				
65 70 75 80				
atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gaa cca agc				288
Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser				
85 90 95				
att tta gcg atc aaa caa caa gtg aaa gat aaa aac gct cct att tta				336
Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu				
100 105 110				
gtg cta ggg aca aaa gcg acg att caa tct aac gct tac gac aac gcc				384
Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala				
115 120 125				
ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt				432
Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu				
130 135 140				
ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg cta gaa				480
Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu				
145 150 155 160				
act tgc atg cgt tat tat ttc act ccc tta aag att tta ccc aaa gta				528
Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Lys Val				
165 170 175				
atc att tta ggt tgc acg cat ttt ccc ttg atc gct cac caa att aag				576
Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Lys				

180	185	190	
ggc tat ttt atg ggg cat ttt gcc ctt tca acg ccc ccc cta ctc atc			624
Gly Tyr Phe Met Gly His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile			
195	200	205	
cat tcg ggc gat gct att gtg gga tat ttg caa caa aaa tac gcc ctt			672
His Ser Gly Asp Ala Ile Val Gly Tyr Leu Gln Gln Lys Tyr Ala Leu			
210	215	220	
aag aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc			720
Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly			
225	230	235	240
gat gtg atc tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa			768
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20	25	30	
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys			
35	40	45	
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu			
50	55	60	
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu			
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Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser			
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Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu			
100	105	110	
Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala			
115	120	125	

Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu  
 130 135 140

Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu  
 145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Lys Val  
 165 170 175

Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Lys  
 180 185 190

Gly Tyr Phe Met Gly His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile  
 195 200 205

His Ser Gly Asp Ala Ile Val Gly Tyr Leu Gln Gln Lys Tyr Ala Leu  
 210 215 220

Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly  
 225 230 235 240

Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu  
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 aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc 96  
 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly  
 20 25 30  
 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag 144  
 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys  
 35 40 45  
 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa 192  
 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys  
 50 55 60  
 tta ttg att gtg gca tgc aac aca gcg agt gct ctg gct tta gaa gag 240

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Met	Gln	Lys	His	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser		288
				85					90					95			
<i>att tta gcg atc aaa caa cag gta aaa gat aaa aac gcc ccc att tta</i>																	
Ile	Leu	Ala	Ile	Lys	Gln	Gln	Val	Lys	Asp	Lys	Asn	Ala	Pro	Ile	Leu		336
				100				105					110				
<i>gtg cta ggc aca aaa gcg acg att caa tct aac gct tac gat aac gct</i>																	
Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Gln	Ser	Asn	Ala	Tyr	Asp	Asn	Ala		384
		115					120					125					
<i>ctg aaa cga caa ggc tat ttg aac gtt tcg cat tta gcc act tcc ctt</i>																	
Leu	Lys	Arg	Gln	Gly	Tyr	Leu	Asn	Val	Ser	His	Leu	Ala	Thr	Ser	Leu		432
		130				135					140						
<i>ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa</i>																	
Phe	Val	Pro	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu		480
145					150					155					160		
<i>act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg</i>																	
Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Lys	Ile	Leu	Pro	Glu	Val		528
				165				170						175			
<i>atc att tta ggt tgt acg cat ttt ccc ttg atc gct caa aaa att gag</i>																	
Ile	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	Gln	Lys	Ile	Glu		576
			180					185					190				
<i>ggc tat ttt atg gaa cat ttt gcc ttt cca acg ccc ccc cta ctc atc</i>																	
Gly	Tyr	Phe	Met	Glu	His	Phe	Ala	Phe	Pro	Thr	Pro	Pro	Pro	Leu	Leu	Ile	624
		195					200					205					
<i>cat tcg ggc gat gct att gtg gaa tat ttg cag caa aaa tac gcc ctt</i>																	
His	Ser	Gly	Asp	Ala	Ile	Val	Glu	Tyr	Leu	Gln	Gln	Lys	Tyr	Ala	Leu		672
		210				215				220							
<i>aag aaa aat gca cac gca tta cct aaa gtg gaa ttt cat gcg agc ggc</i>																	
Lys	Lys	Asn	Ala	His	Ala	Leu	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly		720
225					230					235					240		
<i>gat gtg atc tgg cta gaa aaa caa gct aaa gaa tgg ctc aaa ttg taa</i>																	
Asp	Val	Ile	Trp	Leu	Glu	Lys	Gln	Ala	Lys	Glu	Trp	Leu	Lys	Leu			768
				245					250					255			
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 20 25 30

Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys  
 35 40 45

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys  
 50 55 60

Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu  
 65 70 75 80

Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser  
 85 90 95

Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu  
 100 105 110

Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala  
 115 120 125

Leu Lys Arg Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu  
 130 135 140

Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu  
 145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val  
 165 170 175

Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu  
 180 185 190

Gly Tyr Phe Met Glu His Phe Ala Phe Pro Thr Pro Pro Leu Leu Ile  
 195 200 205

His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu  
 210 215 220

Lys Lys Asn Ala His Ala Leu Pro Lys Val Glu Phe His Ala Ser Gly  
 225 230 235 240

Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu  
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 aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc 96  
 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly  
 20 25 30  
 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag 144  
 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys  
 35 40 45  
 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa 192  
 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys  
 50 55 60  
 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag 240  
 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu  
 65 70 75 80  
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 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser  
 85 90 95  
 att tta gcg atc aaa caa caa gta aag gat aaa aac gcc ccc att tta 336  
 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu  
 100 105 110  
 gtg cta ggg aca aaa gcg acg att caa tct aac gct tac gat aac gct 384  
 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala  
 115 120 125  
 ctg aaa caa caa ggc tat ttg aac gtt tcg cat tta gcc act tct ctt 432  
 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu  
 130 135 140  
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 Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu  
 145 150 155 160  
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 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val  
 165 170 175  
 atc att tta ggt tgc acg cat ttt ccc tta atc gct caa aaa att gag 576



Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu  
 180 185 190

ggc tat ttc atg ggg cat ttt gcc ctt cca acg ccc ccc ata ctc atc 624  
 Gly Tyr Phe Met Gly His Phe Ala Leu Pro Thr Pro Pro Ile Leu Ile  
 195 200 205

cat tct ggc gac gct att gta gaa tat ttg caa caa aaa tac gcc ctt 672  
 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu  
 210 215 220

aag aaa aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc 720  
 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly  
 225 230 235 240

gat atg atc tgg cta gaa aaa caa gct aaa gaa tgg ctc aaa ttg taa 768  
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Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys  
 35 40 45

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys  
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Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu  
 65 70 75 80

Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser  
 85 90 95

Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu  
 100 105 110

Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala  
 115 120 125

Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu  
 130 135 140

Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu  
 145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val  
 165 170 175

Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu  
 180 185 190

Gly Tyr Phe Met Gly His Phe Ala Leu Pro Thr Pro Pro Ile Leu Ile  
 195 200 205

His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu  
 210 215 220

Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly  
 225 230 235 240

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 aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc 96  
 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly  
 20 25 30  
 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag 144  
 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys  
 35 40 45  
 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa 192  
 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys  
 50 55 60

tta ttg att gta gca tgc aac aca gcg agc gct cta gct tta gaa gag	240
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu	
65 70 75 80	
atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc	288
Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser	
85 90 95	
att tta gcg atc aaa caa caa gta aaa gat aaa aac gcc cct att tta	336
Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu	
100 105 110	
gtg cta ggg aca aaa gcg acg att caa tct aac gct tat gac aac gcc	384
Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala	
115 120 125	
ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt	432
Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu	
130 135 140	
ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa	480
Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu	
145 150 155 160	
act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg	528
Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val	
165 170 175	
att att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag	576
Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu	
180 185 190	
agc tat ttt atg ggg cat ttt gcc ctt cca acg ccc ccc cta ctc atc	624
Ser Tyr Phe Met Gly His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile	
195 200 205	
cat tct ggc gat gct att gtg gaa tat ttg cag caa aaa tac gcc ctt	672
His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu	
210 215 220	
aag aaa aac gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc	720
Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly	
225 230 235 240	
gat gtg atc tgg cta gaa aaa caa gct aaa gaa tgg ctc aaa ttg taa	768
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Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys  
 35 40 45

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys  
 50 55 60

Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu  
 65 70 75 80

Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser  
 85 90 95

Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu  
 100 105 110

Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala  
 115 120 125

Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu  
 130 135 140

Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu  
 145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val  
 165 170 175

Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu  
 180 185 190

Ser Tyr Phe Met Gly His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile  
 195 200 205

His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu  
 210 215 220

Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly  
 225 230 235 240

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aaa agc ctt tta aaa gcg caa cta ttt gat gaa atc atc tat tat ggc 96  
 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly  
                   20                  25                  30

gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag 144  
 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys  
                   35                  40                  45

caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gga 192  
 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly  
                   50                  55                  60

tta ttg att gtg gca tgc aac aca gcg agc gct ctg gct tta gaa gag 240  
 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu  
 65                  70                  75                  80

atg caa aaa tat tcc aaa atc cct att gtg ggc gtg att gag cca agc 288  
 Met Gln Lys Tyr Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser  
                   85                  90                  95

att tta gcg atc aaa caa caa gta aaa gat aaa aac gcc ccc att tta 336  
 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu  
                   100                  105                  110

gtg cta ggg aca aaa gcg acg atc caa tct aac gct tat gat aac gcc 384  
 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala  
                   115                  120                  125

ctg aaa caa caa ggc tat ttg aac att tcg cat tta gcc act tct ctt 432  
 Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu  
                   130                  135                  140

ttt gtg ccc ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa 480  
 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu  
 145                  150                  155                  160

act tgc atg cgt tat tat ttc act cca tta gag att tta cct gaa gtg 528  
 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val  
                   165                  170                  175

atc att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag 576  
 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu  
 180 185 190

agc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc tta ctc atc 624  
 Ser Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile  
 195 200 205

cat tct ggc gat gct att gtg gaa tac ttg caa caa aaa tac gcc ctt 672  
 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu  
 210 215 220

aag aaa aac gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc 720  
 Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly  
 225 230 235 240

gat gtg atc tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa 768  
 Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu  
 245 250 255

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Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys  
 35 40 45

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly  
 50 55 60

Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu  
 65 70 75 80

Met Gln Lys Tyr Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser  
 85 90 95

Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu  
 100 105 110

Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala

115	120	125
Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu		
130	135	140
Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu		
145	150	155 160
Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val		
	165	170 175
Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu		
	180	185 190
Ser Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile		
	195	200 205
His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu		
	210	215 220
Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly		
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Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu		
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<221> CDS  
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1 5 10 15	
aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc	96
Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly	
20 25 30	
gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag	144
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys	
35 40 45	
caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac aaa att gaa	192
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Lys Ile Glu	

50	55	60	
tta tta att gtg gca tgc aac aca gcg agc gct ctg gct tta gaa gag			240
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu			
65	70	75	80
atg caa aag cat tcc aaa atc ccc att gtg ggc gtg att gag cca agc			288
Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser			
	85	90	95
att tta gcg atc aaa caa caa gtg aaa gat aaa aac acc cct att tta			336
Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Thr Pro Ile Leu			
	100	105	110
gtg cta ggg aca aaa gcg acg atc caa tct aac gct tac gat aac gcc			384
Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala			
	115	120	125
ctg aaa caa caa ggc tat ttg aag gtt tcg cat ttg gcc act tct ctt			432
Leu Lys Gln Gln Gly Tyr Leu Lys Val Ser His Leu Ala Thr Ser Leu			
	130	135	140
ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa			480
Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu			
	145	150	155
act tgc atg cgt tat tat ttc act cca tta gaa atc tta cct gaa gtg			528
Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val			
	165	170	175
gtt att tta ggc tgc acg cat ttt ccc ttg atc gct caa aaa att gag			576
Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu			
	180	185	190
ggc tat ttt atg gaa cat ttt gcc ctt cca acg ccc ccc cta ctc atc			624
Gly Tyr Phe Met Glu His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile			
	195	200	205
cat tct ggc gac gct att gtg gga tat ttg cag caa aaa tac gcc ctt			672
His Ser Gly Asp Ala Ile Val Gly Tyr Leu Gln Gln Lys Tyr Ala Leu			
	210	215	220
aag aaa aac gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc			720
Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly			
	225	230	235
gat gta att tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa			768
Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu			
	245	250	255

&lt;210&gt; 26

&lt;211&gt; 255

&lt;212&gt; PRT

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&lt;400&gt; 26



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Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly  
 20 25 30

Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys  
 35 40 45

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Lys Ile Glu  
 50 55 60

Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu  
 65 70 75 80

Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser  
 85 90 95

Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Thr Pro Ile Leu  
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Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala  
 115 120 125

Leu Lys Gln Gln Gly Tyr Leu Lys Val Ser His Leu Ala Thr Ser Leu  
 130 135 140

Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu  
 145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val  
 165 170 175

Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu  
 180 185 190

Gly Tyr Phe Met Glu His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile  
 195 200 205

His Ser Gly Asp Ala Ile Val Gly Tyr Leu Gln Gln Lys Tyr Ala Leu  
 210 215 220

Lys Lys Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly

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Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu				
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 aaa agc ctt tta aaa gcg caa att ttt gat gaa atc atc tat tat ggc				
Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly				96
	20	25	30	
 gat agc gct agg gtg cct tat ggc act aaa gac ccc acc acg atc aag				
Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys				144
	35	40	45	
 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac aag att gaa				
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Lys Ile Glu				192
	50	55	60	
 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gaa				
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu				240
	65	70	75	80
 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gaa cca agc				
Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser				288
	85	90	95	
 att tta gcg atc aaa caa caa gta aaa gat aaa aac gcc cct att tta				
Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu				336
	100	105	110	
 gtg cta ggg aca aaa gcg acg att caa tct aac gct tat gac aac gcc				
Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala				384
	115	120	125	
 ctg aaa caa caa ggc tat ttg aat gtt tgc cat tta gcc act tct ctt				
Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu				432
	130	135	140	
 ttt gtg cct ttg att gaa gaa aat att tta gag ggc gaa ttg cta gaa				
Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu				480
	145	150	155	160
 act tgc atg cgt tat tat ttc act cca tta gag atc ttg cct gaa gtg				
Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val				528

165										170					175					
ggt	att	tta	ggc	tgc	acg	cat	ttt	ccc	ttg	atc	gct	cac	caa	att	gag	576				
Val	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	His	Gln	Ile	Glu					
			180					185					190							
ggc	tat	ttt	atg	gag	cat	ttt	gcc	ctt	tca	acg	ccc	ccc	cta	ctc	atc	624				
Gly	Tyr	Phe	Met	Glu	His	Phe	Ala	Leu	Ser	Thr	Pro	Pro	Leu	Leu	Ile					
		195					200				205									
cat	tct	ggc	gat	gct	att	gtg	gaa	tat	ttg	cag	caa	aaa	tac	gcc	ctt	672				
His	Ser	Gly	Asp	Ala	Ile	Val	Glu	Tyr	Leu	Gln	Gln	Lys	Tyr	Ala	Leu					
	210					215				220										
aag	aaa	aac	gca	tgt	gca	ttc	cct	aaa	gta	gaa	ttt	cat	gcg	agc	ggc	720				
Lys	Lys	Asn	Ala	Cys	Ala	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly					
225					230				235						240					
gat	gta	att	tgg	cta	gaa	aaa	cag	gct	aaa	gaa	tgg	ctc	aaa	ttg	taa	768				
Asp	Val	Ile	Trp	Leu	Glu	Lys	Gln	Ala	Lys	Glu	Trp	Leu	Lys	Leu						
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		20						25					30							
Asp	Ser	Ala	Arg	Val	Pro	Tyr	Gly	Thr	Lys	Asp	Pro	Thr	Thr	Ile	Lys					
	35						40					45								
Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Lys	Ile	Glu					
	50					55					60									
Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Glu	Glu					
65					70					75					80					
Met	Gln	Lys	His	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser					
				85					90					95						
Ile	Leu	Ala	Ile	Lys	Gln	Gln	Val	Lys	Asp	Lys	Asn	Ala	Pro	Ile	Leu					
			100					105					110							

Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala  
 115 120 125

Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu  
 130 135 140

Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu  
 145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val  
 165 170 175

Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Glu  
 180 185 190

Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile  
 195 200 205

His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu  
 210 215 220

Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly  
 225 230 235 240

Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu  
 245 250 255

<210> 29  
 <211> 768  
 <212> DNA  
 <213> H. pylori

<221> CDS  
 <222> (1)..(768)

<400> 29  
 atg aaa ata ggc gtt ttt gat agc ggt gtg gga ggg ttt agc gtt tta 48  
 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu  
 1 5 10 15

aaa agc ctt tta aaa gtg caa tta ttt gat gaa atc atc tat tat ggc 96  
 Lys Ser Leu Leu Lys Val Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly  
 20 25 30

gat agt gct agg gtg cct tat ggc act aaa gac ccc acc acg atc aag 144  
 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys  
 35 40 45

caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac aag att gaa 192

Gln	Phe	Gly	Leu	Glu	Ala	Leu	Asp	Phe	Phe	Lys	Pro	His	Lys	Ile	Glu		
50						55					60						
tta	ttg	att	gtg	gca	tgc	aac	aca	gcg	agc	gct	cta	gct	tta	gga	gag	240	
Leu	Leu	Ile	Val	Ala	Cys	Asn	Thr	Ala	Ser	Ala	Leu	Ala	Leu	Gly	Glu		
65					70				75					80			
atg	caa	aag	tat	tcc	aaa	atc	cct	att	gtg	ggc	gtg	att	gag	cca	agc	288	
Met	Gln	Lys	Tyr	Ser	Lys	Ile	Pro	Ile	Val	Gly	Val	Ile	Glu	Pro	Ser		
				85					90					95			
att	tta	gcg	atc	aaa	caa	caa	gta	aaa	gat	aaa	aac	gcc	cct	att	tta	336	
Ile	Leu	Ala	Ile	Lys	Gln	Gln	Val	Lys	Asp	Lys	Asn	Ala	Pro	Ile	Leu		
			100					105						110			
gta	cta	ggg	aca	aaa	gcg	acg	att	cga	tcc	aac	gct	tat	gac	aac	gcc	384	
Val	Leu	Gly	Thr	Lys	Ala	Thr	Ile	Arg	Ser	Asn	Ala	Tyr	Asp	Asn	Ala		
			115				120						125				
ctg	aaa	caa	caa	ggc	tat	ttg	aat	att	tcg	cat	tta	gcc	act	tct	ctt	432	
Leu	Lys	Gln	Gln	Gly	Tyr	Leu	Asn	Ile	Ser	His	Leu	Ala	Thr	Ser	Leu		
			130				135					140					
ttt	gtg	cct	ttg	att	gaa	gaa	aat	att	tta	gag	ggc	gaa	ttg	cta	gaa	480	
Phe	Val	Pro	Leu	Ile	Glu	Glu	Asn	Ile	Leu	Glu	Gly	Glu	Leu	Leu	Glu		
145					150					155					160		
act	tgc	atg	cgt	tat	tat	ttc	act	cca	tta	gag	att	tta	cct	gaa	gtg	528	
Thr	Cys	Met	Arg	Tyr	Tyr	Phe	Thr	Pro	Leu	Glu	Ile	Leu	Pro	Glu	Val		
				165					170					175			
gtt	att	tta	ggt	tgc	acg	cat	ttt	ccc	ttg	atc	gct	cac	caa	att	gag	576	
Val	Ile	Leu	Gly	Cys	Thr	His	Phe	Pro	Leu	Ile	Ala	His	Gln	Ile	Glu		
			180					185						190			
ggc	tat	ttt	atg	gag	cat	ttt	gcc	ctt	tca	acg	ccc	ccc	cta	ctc	atc	624	
Gly	Tyr	Phe	Met	Glu	His	Phe	Ala	Leu	Ser	Thr	Pro	Pro	Leu	Leu	Ile		
			195				200						205				
cat	tct	ggc	gat	gct	att	gtg	gaa	tat	ttg	caa	caa	aaa	tac	gcc	ctt	672	
His	Ser	Gly	Asp	Ala	Ile	Val	Glu	Tyr	Leu	Gln	Gln	Lys	Tyr	Ala	Leu		
			210				215					220					
aag	aaa	aac	gca	tgc	gca	ttc	cct	aaa	gta	gaa	ttc	cat	gcg	agc	ggc	720	
Lys	Lys	Asn	Ala	Cys	Ala	Phe	Pro	Lys	Val	Glu	Phe	His	Ala	Ser	Gly		
225					230					235					240		
gat	gta	att	tgg	cta	gaa	aaa	cag	gct	aaa	gaa	tgg	ctc	aaa	ttg	taa	768	
Asp	Val	Ile	Trp	Leu	Glu	Lys	Gln	Ala	Lys	Glu	Trp	Leu	Lys	Leu			
				245					250					255			

<210> 30  
 <211> 255  
 <212> PRT  
 <213> H. pylori

<400> 30

Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu  
 1 5 10 15

Lys Ser Leu Leu Lys Val Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly  
 20 25 30

Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys  
 35 40 45

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Lys Ile Glu  
 50 55 60

Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Gly Glu  
 65 70 75 80

Met Gln Lys Tyr Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser  
 85 90 95

Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu  
 100 105 110

Val Leu Gly Thr Lys Ala Thr Ile Arg Ser Asn Ala Tyr Asp Asn Ala  
 115 120 125

Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu  
 130 135 140

Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu  
 145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val  
 165 170 175

Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Glu  
 180 185 190

Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile  
 195 200 205

His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu  
 210 215 220

Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly  
 225 230 235 240

Asp Val Ile Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu  
 245 250 255

<210> 31  
 <211> 768  
 <212> DNA  
 <213> H. pylori

<221> CDS  
 <222> (1)..(768)

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 1 5 10 15  
 aaa agc ctt tta aaa gcg caa att ttt gat gaa atc atc tat tat ggc 96  
 Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly  
 20 25 30  
 gat agt gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag 144  
 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys  
 35 40 45  
 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gga 192  
 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly  
 50 55 60  
 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag 240  
 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu  
 65 70 75 80  
 atg caa aag cat tcc aaa atc cct att gtg ggt gtg att gag cca agc 288  
 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser  
 85 90 95  
 att tta gcg atc aaa caa caa gta aaa gat aaa aac gcc cct att tta 336  
 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu  
 100 105 110  
 gtg tta ggg aca aaa gcg acg att caa tcc aac gct tat gac aac gcc 384  
 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala  
 115 120 125  
 ctg aaa caa caa ggc tat ttg aac gtt tcg cat tta gcc act tct ctt 432  
 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu  
 130 135 140  
 ttt gtg cct ttg att gaa gaa aat att tta gag ggc gaa ttg tta gaa 480  
 Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu  
 145 150 155 160  
 act tgc atg cgt tat tat ttc act cca tta gag att tta cct gaa gtg 528

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val  
 165 170 175

gtt att tta ggt tgc acg cat ttt ccc ttg atc gct cac caa att gag 576  
 Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Glu  
 180 185 190

ggc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc tta ctc atc 624  
 Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile  
 195 200 205

cat tct ggc gat gct att gtg gaa tat ttg caa caa aaa tac acc ctt 672  
 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Thr Leu  
 210 215 220

aag aaa aat gca tgc gcg ttc cct aaa gtg gaa ttt cat gcg agc ggc 720  
 Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly  
 225 230 235 240

gat gtg gtt tgg cta gaa aaa cag gct aaa gaa tgg ctc aaa ttg taa 768  
 Asp Val Val Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu  
 245 250 255

<210> 32  
 <211> 255  
 <212> PRT  
 <213> H. pylori

<400> 32

Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu  
 1 5 10 15

Lys Ser Leu Leu Lys Ala Gln Ile Phe Asp Glu Ile Ile Tyr Tyr Gly  
 20 25 30

Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys  
 35 40 45

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Gly  
 50 55 60

Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu  
 65 70 75 80

Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser  
 85 90 95

Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu  
 100 105 110



Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala  
 115 120 125

Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu  
 130 135 140

Phe Val Pro Leu Ile Glu Glu Asn Ile Leu Glu Gly Glu Leu Leu Glu  
 145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val  
 165 170 175

Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala His Gln Ile Glu  
 180 185 190

Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile  
 195 200 205

His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Thr Leu  
 210 215 220

Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly  
 225 230 235 240

Asp Val Val Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu  
 245 250 255

<210> 33  
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 <212> DNA  
 <213> H. pylori

<221> CDS  
 <222> (1)..(765)

<400> 33  
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 Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu  
 1 5 10 15

aaa agc ctt tta aaa gcg caa cta ttt gat gaa atc atc tat tat ggc 96  
 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly  
 20 25 30

gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag 144  
 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys  
 35 40 45

caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att aaa	192
Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys	
50 55 60	
tta ttg att gtg gca tgc aac acc gca agc gct ctg gct tta gaa gag	240
Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu	
65 70 75 80	
atg caa aag cat tcc aaa atc cct gtt gtg ggc gtg att gag cca agc	288
Met Gln Lys His Ser Lys Ile Pro Val Val Gly Val Ile Glu Pro Ser	
85 90 95	
att tta gcg atc aaa cgg caa gtg aaa gat aaa aac gcc cct att ttg	336
Ile Leu Ala Ile Lys Arg Gln Val Lys Asp Lys Asn Ala Pro Ile Leu	
100 105 110	
gtg cta ggg aca aaa gcg acg att caa tcc aac gcc tat gat aac gcc	384
Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala	
115 120 125	
ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt	432
Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu	
130 135 140	
ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg cta gaa	480
Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu	
145 150 155 160	
act tgc atg cgt tat tat ttc act cca tta gag att tta cct gaa gtg	528
Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val	
165 170 175	
gtt att tta ggt tgc acg cat ttt ccc ttg atc gct caa aaa att gag	576
Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu	
180 185 190	
ggc tat ttt atg gag cat ttt gcc ctt tca acg ccc ccc cta ctc atc	624
Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile	
195 200 205	
cat tct ggc gat gct att gtg gaa tat ttg caa caa aat tac gcc ctt	672
His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Asn Tyr Ala Leu	
210 215 220	
aag aaa aac gca tgc gcg ttc cct aaa gtg gaa ttt cat gcg agc ggc	720
Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly	
225 230 235 240	
gat gtg gtt tgg cta gaa aaa caa gct aaa gaa tgg ctt aaa ttg	765
Asp Val Val Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu	
245 250 255	
<210> 34	
<211> 255	
<212> PRT	
<213> H. pylori	

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Met Lys Ile Gly Val Phe Asp Ser Gly Val Gly Gly Phe Ser Val Leu  
 1 5 10 15

Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly  
 20 25 30

Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys  
 35 40 45

Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Lys  
 50 55 60

Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu  
 65 70 75 80

Met Gln Lys His Ser Lys Ile Pro Val Val Gly Val Ile Glu Pro Ser  
 85 90 95

Ile Leu Ala Ile Lys Arg Gln Val Lys Asp Lys Asn Ala Pro Ile Leu  
 100 105 110

Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala  
 115 120 125

Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu  
 130 135 140

Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu  
 145 150 155 160

Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val  
 165 170 175

Val Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu  
 180 185 190

Gly Tyr Phe Met Glu His Phe Ala Leu Ser Thr Pro Pro Leu Leu Ile  
 195 200 205

His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Asn Tyr Ala Leu  
 210 215 220

Lys Lys Asn Ala Cys Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly  
 225 230 235 240

Asp Val Val Trp Leu Glu Lys Gln Ala Lys Glu Trp Leu Lys Leu  
 245 250 255

<210> 35  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Homo sapiens

<400> 35  
 aaatagtcac atgaaaatag gcgttttttg 29

<210> 36  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Homo sapiens

<400> 36  
 agaattctat tacaatttga gccattct 28

<210> 37  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Homo sapiens

<400> 37  
 gcgaattcga tcagaatttt ttttct 26

<210> 38  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Homo sapiens

<400> 38  
 ataagtactt gtgaatctta tactag 26

<210> 39  
 <211> 858  
 <212> DNA  
 <213> E. coli

<400> 39  
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cgtcccaccg tgctgggtgtt tgactccggc gtcgggtgggt tgtcgggtcta tgacgagatc 120  
cggcatctct taccggatct ccattacatt tatgctttcg ataacgtcgc tttcccgtat 180  
ggcgaaaaaa gcgaagcgtt tattgttgag cgagtgggtg caattgtcac cgcggtgcaa 240  
gaacgttatc cccttgcgct ggctgtggtc gcttgcaaca ctgccagtac cgtttcactt 300  
cctgcattac gcgaaaagtt cgacttcccg gttgttggtg tcgtgccggc gattaaacct 360  
gctgcacgtc tgacggcaaa tggcattgtc ggattactgg caaccgcgg aacagttaaa 420  
cgttcttata ctcatgagct gatcgcgcgt ttcgctaata aatgccagat agaaatgctg 480  
ggctcggcag agatgggtga gttggctgaa gcgaagctac atggcgaaga tgtttctctg 540  
gatgcactaa aacgtatcct acgcccgtgg ttaagaatga aagagccgcc agataccgtt 600  
gtattgggtt gcacccatct ccctctacta caagaagaac tgttacaagt gctgccagag 660  
ggaacccggc tgggtggattc tggcgcagcg attgctcgcc gaacggcctg gttgttagaa 720  
catgaagccc cggatgcaaa atctgccgat gcgaatattg ccttttgtat ggcaatgacg 780  
ccaggagctg aacaattatt gcccgtttta cagcgttacg gcttcgaaac gctcgaaaaa 840  
ctggcagttt taggctga 858

<210> 40  
<211> 285  
<212> PRT  
<213> E. coli

<400> 40

Met Ala Thr Lys Leu Gln Asp Gly Asn Thr Pro Cys Leu Ala Ala Thr  
1 5 10 15

Pro Ser Glu Pro Arg Pro Thr Val Leu Val Phe Asp Ser Gly Val Gly  
20 25 30

Gly Leu Ser Val Tyr Asp Glu Ile Arg His Leu Leu Pro Asp Leu His  
35 40 45

Tyr Ile Tyr Ala Phe Asp Asn Val Ala Phe Pro Tyr Gly Glu Lys Ser  
50 55 60

Glu Ala Phe Ile Val Glu Arg Val Val Ala Ile Val Thr Ala Val Gln  
65 70 75 80

Glu Arg Tyr Pro Leu Ala Leu Ala Val Val Ala Cys Asn Thr Ala Ser  
85 90 95

Thr Val Ser Leu Pro Ala Leu Arg Glu Lys Phe Asp Phe Pro Val Val  
100 105 110

Gly Val Val Pro Ala Ile Lys Pro Ala Ala Arg Leu Thr Ala Asn Gly  
115 120 125

Ile Val Gly Leu Leu Ala Thr Arg Gly Thr Val Lys Arg Ser Tyr Thr  
130 135 140

His Glu Leu Ile Ala Arg Phe Ala Asn Glu Cys Gln Ile Glu Met Leu  
145 150 155 160

Gly Ser Ala Glu Met Val Glu Leu Ala Glu Ala Lys Leu His Gly Glu  
165 170 175

Asp Val Ser Leu Asp Ala Leu Lys Arg Ile Leu Arg Pro Trp Leu Arg  
180 185 190

Met Lys Glu Pro Pro Asp Thr Val Val Leu Gly Cys Thr His Phe Pro  
195 200 205

Leu Leu Gln Glu Glu Leu Leu Gln Val Leu Pro Glu Gly Thr Arg Leu  
210 215 220

Val Asp Ser Gly Ala Ala Ile Ala Arg Arg Thr Ala Trp Leu Leu Glu  
225 230 235 240

His Glu Ala Pro Asp Ala Lys Ser Ala Asp Ala Asn Ile Ala Phe Cys  
245 250 255

Met Ala Met Thr Pro Gly Ala Glu Gln Leu Leu Pro Val Leu Gln Arg  
260 265 270

Tyr Gly Phe Glu Thr Leu Glu Lys Leu Ala Val Leu Gly  
275 280 285

<210> 41

<211> 29

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Homo sapiens

&lt;400&gt; 41

aaatagtcac atgaaaatag gcgtttttg 29

&lt;210&gt; 42

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Homo sapiens

&lt;400&gt; 42

agaattctat tacaatttga gccattct 28

&lt;210&gt; 43

&lt;211&gt; 822

&lt;212&gt; DNA

&lt;213&gt; E. faecalis

&lt;400&gt; 43

atgagcaatc aagaagccat tggattaatt gattctggcg ttggtggatt aactgtttta 60

aaggaagcgc taaagcaatt accaaatgaa cgattaattt atttaggaga tacagcccg 120

tgcccatatg gtccacgacc agccgaacaa gtcgttcagt ttacttggga aatggccgat 180

tttttattga aaaaacgaat aaaaatgcta gtaatcgcat gtaataccgc gacggctgtc 240

gcattagaag aaattaaagc tgccttgcca attccagttg ttggtgttat ttacctggc 300

gcacgagcag ccgttaaagt cacaaaaaat aacaaaattg gtgtcatagg taccttaggg 360

acaatcaaaa gtgcttccta tgaaatcgcc attaaaagta aggcaccagc aattgaggtg 420

actagtttag cttgccctaa atttgtcccc attgttgaaa gtaatcaata tcgttcttcc 480

gtagcaaaaa aaattgtggc agaaacactt caagcactac aattaaaagg acttgatacg 540

ttgatttttag gttgtaccca ttaccggttg ttacgtccgg tgattcaaaa tgtgatggg 600

agtcatttga cattaattga ctcaggagcc gaaacagttg gcgaagtcag catgcttctc 660

gattattttg acattgcca cagcctgaa gcgcctacac agcccatga atttataca 720

actggttctg caaaaatgtt tgaagagatt gcaagcagtt ggcttggtat agagaactta 780

aaagcacaac agattcactt aggaggaaac gaaaatgatt ag 822

&lt;210&gt; 44

&lt;211&gt; 273

&lt;212&gt; PRT

&lt;213&gt; E. faecalis

&lt;400&gt; 44

Met Ser Asn Gln Glu Ala Ile Gly Leu Ile Asp Ser Gly Val Gly Gly  
 1 5 10 15

Leu Thr Val Leu Lys Glu Ala Leu Lys Gln Leu Pro Asn Glu Arg Leu  
 20 25 30

Ile Tyr Leu Gly Asp Thr Ala Arg Cys Pro Tyr Gly Pro Arg Pro Ala  
 35 40 45

Glu Gln Val Val Gln Phe Thr Trp Glu Met Ala Asp Phe Leu Leu Lys  
 50 55 60

Lys Arg Ile Lys Met Leu Val Ile Ala Cys Asn Thr Ala Thr Ala Val  
 65 70 75 80

Ala Leu Glu Glu Ile Lys Ala Ala Leu Pro Ile Pro Val Val Gly Val  
 85 90 95

Ile Leu Pro Gly Ala Arg Ala Ala Val Lys Val Thr Lys Asn Asn Lys  
 100 105 110

Ile Gly Val Ile Gly Thr Leu Gly Thr Ile Lys Ser Ala Ser Tyr Glu  
 115 120 125

Ile Ala Ile Lys Ser Lys Ala Pro Ala Ile Glu Val Thr Ser Leu Ala  
 130 135 140

Cys Pro Lys Phe Val Pro Ile Val Glu Ser Asn Gln Tyr Arg Ser Ser  
 145 150 155 160

Val Ala Lys Lys Ile Val Ala Glu Thr Leu Gln Ala Leu Gln Leu Lys  
 165 170 175

Gly Leu Asp Thr Leu Ile Leu Gly Cys Thr His Tyr Pro Leu Leu Arg  
 180 185 190

Pro Val Ile Gln Asn Val Met Gly Ser His Val Thr Leu Ile Asp Ser  
 195 200 205

Gly Ala Glu Thr Val Gly Glu Val Ser Met Leu Leu Asp Tyr Phe Asp  
 210 215 220



Ile Ala His Thr Pro Glu Ala Pro Thr Gln Pro His Glu Phe Tyr Thr  
 225 230 235 240

Thr Gly Ser Ala Lys Met Phe Glu Glu Ile Ala Ser Ser Trp Leu Gly  
 245 250 255

Ile Glu Asn Leu Lys Ala Gln Gln Ile His Leu Gly Gly Asn Glu Asn  
 260 265 270

Asp

<210> 45  
 <211> 801  
 <212> DNA  
 <213> S. aureus

<400> 45  
 atgaataaac caataggtgt aatagactct ggtgtcggag gtttgacagt agctaaagaa 60  
 attatgcgtc agttgccaaa tgagacgatt tattacttag gtgatattgg gcgatgtcca 120  
 tatgggccaa gaccaggaga acaagtaaaa caatatacag ttgaaatcgc tcgtaaatta 180  
 atggaatttg atataaaaaat gtcctgtgatt gcttgtaata ctgcaactgc tgtagcttta 240  
 gaatatttac aaaagacctt atcaatctca gtgattggcg taattgaacc aggtgctaga 300  
 acagcaataa tgacgactag aaatcaaaaat gtattagtag taggaacgga aggacacaatt 360  
 aaatctgaag catatcgaac acatattaaa cgtataaatc cacatgtaga ggtacatggc 420  
 gttgcctgtc cagggtttgt gccacttgta gaacaaatga gatatagtga tccaacaatt 480  
 acaagcattg ttattcatca aacactgaaa cgttggcgta atagttagtc tgatactgtc 540  
 attttaggat gtaccacta tccattgctc tataaaccta tctatgatta ttttggtggt 600  
 aaaaagacag tgatttcgtc tggattagaa acggctcgtg aagttagtgc attgctaaca 660  
 tttagtaatg aacatgcaag ttatactgaa catccagatc atcgatTTTT tgcaacaggt 720  
 gataccacac atattactaa cattatcaaa gaatggctaa atttatctgt caatgtggaa 780  
 cgtatatcag tgaatgacta g 801

<210> 46  
 <211> 266  
 <212> PRT  
 <213> S. aureus

<400> 46

Met Asn Lys Pro Ile Gly Val Ile Asp Ser Gly Val Gly Gly Leu Thr

1	5	10	15
Val Ala Lys Glu Ile Met Arg Gln Leu Pro Asn Glu Thr Ile Tyr Tyr	20	25	30
Leu Gly Asp Ile Gly Arg Cys Pro Tyr Gly Pro Arg Pro Gly Glu Gln	35	40	45
Val Lys Gln Tyr Thr Val Glu Ile Ala Arg Lys Leu Met Glu Phe Asp	50	55	60
Ile Lys Met Leu Val Ile Ala Cys Asn Thr Ala Thr Ala Val Ala Leu	65	70	75
Glu Tyr Leu Gln Lys Thr Leu Ser Ile Ser Val Ile Gly Val Ile Glu	85	90	95
Pro Gly Ala Arg Thr Ala Ile Met Thr Thr Arg Asn Gln Asn Val Leu	100	105	110
Val Leu Gly Thr Glu Gly Thr Ile Lys Ser Glu Ala Tyr Arg Thr His	115	120	125
Ile Lys Arg Ile Asn Pro His Val Glu Val His Gly Val Ala Cys Pro	130	135	140
Gly Phe Val Pro Leu Val Glu Gln Met Arg Tyr Ser Asp Pro Thr Ile	145	150	155
Thr Ser Ile Val Ile His Gln Thr Leu Lys Arg Trp Arg Asn Ser Glu	165	170	175
Ser Asp Thr Val Ile Leu Gly Cys Thr His Tyr Pro Leu Leu Tyr Lys	180	185	190
Pro Ile Tyr Asp Tyr Phe Gly Gly Lys Lys Thr Val Ile Ser Ser Gly	195	200	205
Leu Glu Thr Ala Arg Glu Val Ser Ala Leu Leu Thr Phe Ser Asn Glu	210	215	220
His Ala Ser Tyr Thr Glu His Pro Asp His Arg Phe Phe Ala Thr Gly	225	230	235
			240

Asp Thr Thr His Ile Thr Asn Ile Ile Lys Glu Trp Leu Asn Leu Ser  
245 250 255

Val Asn Val Glu Arg Ile Ser Val Asn Asp  
260 265

<210>	47
<211>	822
<212>	DNA
<213>	<i>E. faecium</i>

<400>	47						
atgatacga	t	gacagataa	tcgccctatc	ggattttattg	attcagggtgt	cggcggccttg	60
actgtagtaa	a	aagaagccct	gaaacaatta	ccgaatgaaa	atatttttatt	tgtaggagac	120
acagcacgct	g	cccatatgg	ccctagaccc	gcggaacagg	taatccagta	tacttgggaa	180
atgacggatt	a	tctgggtgga	gcaaggaatc	aagatgctgg	tgatcgccctg	caataccgca	240
actgcggtgg	c	ttttagaaga	aatcaaagct	gctcttttcta	ttccagtcac	cgggtgtgatc	300
cttcccggta	c	tagagcggc	agtaaaaaaa	acacaaaata	aacaagttgg	cattatcggt	360
acgattggta	c	ggtaaaaaag	tcaagcttat	gaaaaagcac	tgaaagagaa	agtaccagaa	420
ttgactgtga	c	aagtcttgc	ttgtccaaaa	tttgtttcag	ttgtcgaaaag	taatgaatac	480
cattcatcgg	t	ggcgaaaaaa	aattgtggca	gaaacattag	ctcctttaac	cactaaaaaa	540
atcgatacat	t	gatttttggg	atgcacccat	tatccattat	tacgccccat	cattcaaaat	600
gtaatgggag	a	aaatgttca	actgatcgat	tctggagcag	aaacagtagg	tgaagtatct	660
atgctgttag	a	ttattttcaa	tctgagcaat	tcaccgcaaa	atggtcggac	attatgccag	720
ttttatacaa	c	tggctctgc	caaacttttc	gaggaaatag	ctgaagactg	gcttggaatc	780
ggacacttaa	a	tgtagaaca	tatcgaattg	ggaggaaaaat	aa		822

<210>	48
<211>	273
<212>	PRT
<213>	E. faecium

<400> 48

Met Ile Arg Leu Thr Asp Asn Arg Pro Ile Gly Phe Ile Asp Ser Gly  
1 5 10 15

Val Gly Gly Leu Thr Val Val Lys Glu Ala Leu Lys Gln Leu Pro Asn  
20 25 30

Glu Asn Ile Leu Phe Val Gly Asp Thr Ala Arg Cys Pro Tyr Gly Pro  
 35 40 45

Arg Pro Ala Glu Gln Val Ile Gln Tyr Thr Trp Glu Met Thr Asp Tyr  
 50 55 60

Leu Val Glu Gln Gly Ile Lys Met Leu Val Ile Ala Cys Asn Thr Ala  
 65 70 75 80

Thr Ala Val Ala Leu Glu Glu Ile Lys Ala Ala Leu Ser Ile Pro Val  
 85 90 95

Ile Gly Val Ile Leu Pro Gly Thr Arg Ala Ala Val Lys Lys Thr Gln  
 100 105 110

Asn Lys Gln Val Gly Ile Ile Gly Thr Ile Gly Thr Val Lys Ser Gln  
 115 120 125

Ala Tyr Glu Lys Ala Leu Lys Glu Lys Val Pro Glu Leu Thr Val Thr  
 130 135 140

Ser Leu Ala Cys Pro Lys Phe Val Ser Val Val Glu Ser Asn Glu Tyr  
 145 150 155 160

His Ser Ser Val Ala Lys Lys Ile Val Ala Glu Thr Leu Ala Pro Leu  
 165 170 175

Thr Thr Lys Lys Ile Asp Thr Leu Ile Leu Gly Cys Thr His Tyr Pro  
 180 185 190

Leu Leu Arg Pro Ile Ile Gln Asn Val Met Gly Glu Asn Val Gln Leu  
 195 200 205

Ile Asp Ser Gly Ala Glu Thr Val Gly Glu Val Ser Met Leu Leu Asp  
 210 215 220

Tyr Phe Asn Leu Ser Asn Ser Pro Gln Asn Gly Arg Thr Leu Cys Gln  
 225 230 235 240

Phe Tyr Thr Thr Gly Ser Ala Lys Leu Phe Glu Glu Ile Ala Glu Asp  
 245 250 255

Trp Leu Gly Ile Gly His Leu Asn Val Glu His Ile Glu Leu Gly Gly  
 260 265 270

Lys

<210> 49  
 <211> 335  
 <212> DNA  
 <213> E. saccharolyticus

<400> 49  
 gcatgtaata ccgcaacggc ggtagcgta gaagaaatta aagcgcaatt agatattcca 60  
 gtcgtcgggtg tgatcttacc tgggtactcgt gctgcagtta aagctacgaa aaatcgtcaa 120  
 atcgggtatta taggaacagc ggggtacaatt aaaagtagtt cgtatgagca agcaattaaa 180  
 atgaaagtgc ctgaagcatc ggtgactagt ttagcttgct ctaaatttgt accgattggt 240  
 gaaagtaatc aatttcaatc atcggtagct aaaaaaattg ttgctgagac gttattacca 300  
 ttgcaacata aaaaattaga tacgttgatt ttagg 335

<210> 50  
 <211> 111  
 <212> PRT  
 <213> E. saccharolyticus

<400> 50

Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Glu Glu Ile Lys Ala Gln  
 1 5 10 15

Leu Asp Ile Pro Val Val Gly Val Ile Leu Pro Gly Thr Arg Ala Ala  
 20 25 30

Val Lys Ala Thr Lys Asn Arg Gln Ile Gly Ile Ile Gly Thr Ala Gly  
 35 40 45

Thr Ile Lys Ser Ser Ser Tyr Glu Gln Ala Ile Lys Met Lys Val Pro  
 50 55 60

Glu Ala Ser Val Thr Ser Leu Ala Cys Pro Lys Phe Val Pro Ile Val  
 65 70 75 80

Glu Ser Asn Gln Phe Gln Ser Ser Val Ala Lys Lys Ile Val Ala Glu  
 85 90 95

Thr Leu Leu Pro Leu Gln His Lys Lys Leu Asp Thr Leu Ile Leu  
 100 105 110

<210> 51  
 <211> 344  
 <212> DNA  
 <213> E. mundtii

<400> 51  
 gtaatcgcat gtaataccgc aactgcggtc gcattagaag aaatcaaagc aacactctcg 60  
 attccagtga tcggtgtgat tttgccagga acgagagcgg cagtcaagca gacgaaaaat 120  
 catcgagtag ggggtgattgg aacaattgg accgtcaaaa gtgctgctta cgagacggca 180  
 ttattggata aagcacccga actgaaagtt accagcttgg cgtgtccaaa gtttgtttca 240  
 gtcgtagaaa gtaaagaata ccgatcatca gtcgctaaaa aaatcgtggc tcaaactttg 300  
 cttccattag aattaaaggg gatcgatacg ttgatttttag gttg 344

<210> 52  
 <211> 113  
 <212> PRT  
 <213> E. mundtii

<400> 52

Val Ile Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Glu Glu Ile Lys  
 1 5 10 15

Ala Thr Leu Ser Ile Pro Val Ile Gly Val Ile Leu Pro Gly Thr Arg  
 20 25 30

Ala Ala Val Lys Gln Thr Lys Asn His Arg Val Gly Val Ile Gly Thr  
 35 40 45

Ile Gly Thr Val Lys Ser Ala Ala Tyr Glu Thr Ala Leu Leu Asp Lys  
 50 55 60

Ala Pro Glu Leu Lys Val Thr Ser Leu Ala Cys Pro Lys Phe Val Ser  
 65 70 75 80

Val Val Glu Ser Lys Glu Tyr Arg Ser Ser Val Ala Lys Lys Ile Val  
 85 90 95

Ala Gln Thr Leu Leu Pro Leu Glu Leu Lys Gly Ile Asp Thr Leu Ile  
 100 105 110

Leu

<210> 53

<211> 340  
 <212> DNA  
 <213> E. casseliflavus

<400> 53  
 atcgcatgta ataccgcgac agcggtcgcc cttgaagaaa tcaaagaaca actaacgatc 60  
 ccagtgatcg gcgtgatcct gcctggcagt cgagcagcag tcaaagcaag caaaaaccaa 120  
 cgaatcgggtg tcatcgggac aaacggaacg atcaaaagtg actcttataa gcgcgcgctt 180  
 catggcaaaag cgcccatgc gtccgtcgtc agtttggctt gcccgagtt tgtgccgatc 240  
 gtagaaagca aacaatacca tagctcggtc gccaaagaaa tcgtggcaga aacgttgcgt 300  
 ccattgaaaa acaaacggct agatacgttg attttaggtg 340

<210> 54  
 <211> 112  
 <212> PRT  
 <213> E. casseliflavus

<400> 54  
 Ile Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Glu Glu Ile Lys Glu  
 1 5 10 15  
 Gln Leu Thr Ile Pro Val Ile Gly Val Ile Leu Pro Gly Ser Arg Ala  
 20 25 30  
 Ala Val Lys Ala Ser Lys Asn Gln Arg Ile Gly Val Ile Gly Thr Asn  
 35 40 45  
 Gly Thr Ile Lys Ser Asp Ser Tyr Lys Arg Ala Leu His Gly Lys Ala  
 50 55 60  
 Pro His Ala Ser Val Val Ser Leu Ala Cys Pro Lys Phe Val Pro Ile  
 65 70 75 80  
 Val Glu Ser Lys Gln Tyr His Ser Ser Val Ala Lys Lys Ile Val Ala  
 85 90 95  
 Glu Thr Leu Arg Pro Leu Lys Asn Lys Arg Leu Asp Thr Leu Ile Leu  
 100 105 110

<210> 55  
 <211> 337  
 <212> DNA  
 <213> E. flavescens

<400> 55

atcgcatgta ataccgcgac agcggtcgcc cttgaagaaa tcaaagaaca actaacgatac 60  
 ccagtgatcg gcgtgatcct gcctggcagt cgagcagcag tcaaagcaag caaaaaccaa 120  
 cgaatcgggtg tcatcggggac aaacggaacg atcaaaagtg actcttataa gcgcgcgctt 180  
 catggcaaag cgccccatgc gtccgtcgtc agtttggctt gcccgaaagt tgtgccgatac 240  
 gtagaaaagca aacaatacca tagctcggtc gccaaagaaa tcgtggcaga aacgttgcgt 300  
 ccattgaaaa acaaacggct agatacgttg attttag 337

<210> 56  
 <211> 112  
 <212> PRT  
 <213> E. flavescens

<400> 56

Ile Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Glu Glu Ile Lys Glu  
 1 5 10 15

Gln Leu Thr Ile Pro Val Ile Gly Val Ile Leu Pro Gly Ser Arg Ala  
 20 25 30

Ala Val Lys Ala Ser Lys Asn Gln Arg Ile Gly Val Ile Gly Thr Asn  
 35 40 45

Gly Thr Ile Lys Ser Asp Ser Tyr Lys Arg Ala Leu His Gly Lys Ala  
 50 55 60

Pro His Ala Ser Val Val Ser Leu Ala Cys Pro Lys Phe Val Pro Ile  
 65 70 75 80

Val Glu Ser Lys Gln Tyr His Ser Ser Val Ala Lys Lys Ile Val Ala  
 85 90 95

Glu Thr Leu Arg Pro Leu Lys Asn Lys Arg Leu Asp Thr Leu Ile Leu  
 100 105 110

<210> 57  
 <211> 341  
 <212> DNA  
 <213> E. cecorum

<400> 57

atcgcatgta ataccgcgac tgcagcagct ttaaccctaaa ttaaggaaca attagacatt 60  
 ccagttgtcg gtgtgatttt acctggaact agagctgctg tcaaaaatac aaaatcgcaa 120  
 cgaattggga ttatcggcac acaaggaacc atccaaagtg gcagttatga acaagccatt 180



ctttctaaag taccgactgc tcaacctgtg agtttagcgt gtcctagatt tgttccgata 240  
 gtagaaaagta atcaagcaaa ttcaagtgtg gcaaaaaaaaaa ttgtcgctca aacactacaa 300  
 ccgatgacga aaaaaaacat cgatacgttg atttttaggtt g 341

<210> 58  
 <211> 112  
 <212> PRT  
 <213> E. cecorum

<400> 58

Ile Ala Cys Asn Thr Ala Thr Ala Ala Ala Leu Thr Gln Ile Lys Glu  
 1 5 10 15

Gln Leu Asp Ile Pro Val Val Gly Val Ile Leu Pro Gly Thr Arg Ala  
 20 25 30

Ala Val Lys Asn Thr Lys Ser Gln Arg Ile Gly Ile Ile Gly Thr Gln  
 35 40 45

Gly Thr Ile Gln Ser Gly Ser Tyr Glu Gln Ala Ile Leu Ser Lys Val  
 50 55 60

Pro Thr Ala Gln Pro Val Ser Leu Ala Cys Pro Arg Phe Val Pro Ile  
 65 70 75 80

Val Glu Ser Asn Gln Ala Asn Ser Ser Val Ala Lys Lys Ile Val Ala  
 85 90 95

Gln Thr Leu Gln Pro Met Thr Lys Lys Asn Ile Asp Thr Leu Ile Leu  
 100 105 110

<210> 59  
 <211> 339  
 <212> DNA  
 <213> E. raffinosus

<400> 59

atcgcatgta ataccgcgac ggtagtagct ttggaagaaa ttaaaagaac cgtagatatt 60  
 cccgtaatcg gtgttatata gccaggatct cgcgcagcgt taaaggcaag cgaaaatggg 120  
 cgcgtgggaa ttatcggaac cattggaaca gtaaaaagtgt gttcttataa acacgaacta 180  
 caggaaaaag ctctgatac ttatgtttct agtttagcat gcccaaaatt tgtaccgatt 240  
 gttgaaagta atcaatttaa tagctcggtg gcgaaaaaaaaa ttgtttctca aacattaact 300

cctttgaaaa aggaaaagtt ggatacgttg atttttaggt

339

<210> 60  
 <211> 112  
 <212> PRT  
 <213> E. raffinosus

<400> 60

Ile Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Glu Glu Ile Lys Arg  
 1 5 10 15

Thr Val Asp Ile Pro Val Ile Gly Val Ile Gln Pro Gly Ser Arg Ala  
 20 25 30

Ala Leu Lys Ala Ser Glu Asn Gly Arg Val Gly Ile Ile Gly Thr Ile  
 35 40 45

Gly Thr Val Lys Ser Gly Ser Tyr Lys His Glu Leu Gln Glu Lys Ala  
 50 55 60

Pro Asp Thr Tyr Val Ser Ser Leu Ala Cys Pro Lys Phe Val Pro Ile  
 65 70 75 80

Val Glu Ser Asn Gln Phe Asn Ser Ser Val Ala Lys Lys Ile Val Ser  
 85 90 95

Gln Thr Leu Thr Pro Leu Lys Lys Glu Lys Leu Asp Thr Leu Ile Leu  
 100 105 110

<210> 61  
 <211> 341  
 <212> DNA  
 <213> E. malodoratus

<400> 61

atcgcatgta ataccgcaac cgcagtggtt ttagaagaga ttaagaagaa cgttgatatt 60

cctgttattg gtgttatcca accaggatca cgtgctgcat taaaagcaag taaaaatagt 120

cgtgtaggta tcatcggaac actaggaact gttaaaagtg gatcttataa acatgagctg 180

caagaaaaag caccagaaac gtatgttgct agtctggcct gcccaaaatt tgtgccaatc 240

gttgaaagta atcagtttaa tagttctgta gccaaaaaga ttgtttcaca atctctggca 300

cccttaaaaa aggaaaaatt agatacgttg atttttaggtt g 341

<210> 62  
 <211> 112  
 <212> PRT

<213> E. malodoratus

<400> 62

Ile Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Glu Glu Ile Lys Lys  
1 5 10 15

Asn Val Asp Ile Pro Val Ile Gly Val Ile Gln Pro Gly Ser Arg Ala  
20 25 30

Ala Leu Lys Ala Ser Lys Asn Ser Arg Val Gly Ile Ile Gly Thr Leu  
35 40 45

Gly Thr Val Lys Ser Gly Ser Tyr Lys His Glu Leu Gln Glu Lys Ala  
50 55 60

Pro Glu Thr Tyr Val Ala Ser Leu Ala Cys Pro Lys Phe Val Pro Ile  
65 70 75 80

Val Glu Ser Asn Gln Phe Asn Ser Ser Val Ala Lys Lys Ile Val Ser  
85 90 95

Gln Ser Leu Ala Pro Leu Lys Lys Glu Lys Leu Asp Thr Leu Ile Leu  
100 105 110

<210> 63

<211> 338

<212> DNA

<213> E. solitarus

<400> 63

gcatgtaata cgcgaacagc tgtggcttta gatgagatta aagagcaact gcaaatccct 60

gttggtgggag ttattatgcc gggaaccaga gcagctgtta aagcgactaa aaatcatcgt 120

attggtgtga ttggcacaaa aggaacagtt aaaagtgcct cttacaaacg agcaatcaaa 180

gaaaaaaatg aaaatacaaa agtaacaagt ttggcttgtc cgaagtttgt tcccattgtg 240

gaaagtaatc aaattcattc ttcagtggca aaaaaaattg tatttgaaac actattaccc 300

ttaaaaaata aacatttaga tacgttgatt ttaggttg 338

<210> 64

<211> 111

<212> PRT

<213> E. solitarus

<400> 64

Ala Cys Asn Thr Ala Thr Ala Val Ala Leu Asp Glu Ile Lys Glu Gln

1	5	10	15
Leu Gln Ile	Pro Val Val Gly Val	Ile Met Pro Gly Thr	Arg Ala Ala
	20	25	30
Val Lys Ala	Thr Lys Asn His	Arg Ile Gly Val	Ile Gly Thr Lys Gly
	35	40	45
Thr Val Lys	Ser Ala Ser Tyr	Lys Arg Ala Ile	Lys Glu Lys Asn Glu
	50	55	60
Asn Thr Lys	Val Thr Ser Leu	Ala Cys Pro Lys	Phe Val Pro Ile Val
	65	70	75
Glu Ser Asn	Gln Ile His Ser	Ser Val Ala Lys	Lys Ile Val Phe Glu
	85	90	95
Thr Leu Leu	Pro Leu Lys Asn	Lys His Leu Asp	Thr Leu Ile Leu
	100	105	110

<210> 65  
 <211> 341  
 <212> DNA  
 <213> E. hirae

<400> 65  
 atcgcatgta ataccgctac tgcggttgct ttagaagaaa tcaaggcggc acttcctatt 60  
 ccagtcattg gtgtgatctt acctgggaca agagcagctg ttaaacaaac aagaaataaa 120  
 caagtaggga ttatcggaac cctcggaacg atcaaaagtc gtgcttatga aacagcgctg 180  
 aaaacgaagg tacctgaact tgccgtgact agtttggtt gtccaaaatt cgtttcggta 240  
 gtggaaagta atgaatatca ttcgtcagtg gcaaaaaaaaa tcgttgccca gacactagcg 300  
 ccattgggta ctaagaaaat cgatacggtg attttaggtt g 341

<210> 66  
 <211> 111  
 <212> PRT  
 <213> E. hirae

<400> 66

Ala Cys Asn	Thr Ala Thr	Ala Val Ala	Leu Glu Glu	Ile Lys Ala	Ala
1	5	10	15		

Leu Pro Ile	Pro Val Ile	Gly Val Ile	Leu Pro Gly	Thr Arg Ala	Ala
20	25	30			

Val Lys Gln Thr Arg Asn Lys Gln Val Gly Ile Ile Gly Thr Leu Gly  
 35 40 45

Thr Ile Lys Ser Arg Ala Tyr Glu Thr Ala Leu Lys Thr Lys Val Pro  
 50 55 60

Glu Leu Ala Val Thr Ser Leu Ala Cys Pro Lys Phe Val Ser Val Val  
 65 70 75 80

Glu Ser Asn Glu Tyr His Ser Ser Val Ala Lys Lys Ile Val Ala Gln  
 85 90 95

Thr Leu Ala Pro Leu Val Thr Lys Lys Ile Asp Thr Leu Ile Leu  
 100 105 110

<210> 67  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Homo sapiens

<400> 67  
 aaatagtcac atgaaaatag gcgtttttg 29

<210> 68  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Homo sapiens

<400> 68  
 agaattctat tacaatttga gccattct 28

<210> 69  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Homo sapiens

<400> 69  
 gcgaattcga tcagaatttt ttttct 26

<210> 70  
 <211> 26  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Homo sapiens

<400> 70

ataagtactt gtgaatctta tactag

26

<210> 71

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Homo sapiens

<400> 71

aaaatgctag taatcgcatg taataccgc

29

<210> 72

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Homo sapiens

<400> 72

tgggtacaac ctaaaatcaa cgtatc

26

<210> 73

<211> 765

<212> DNA

<213> Aquifex pyrophilus NA sequence

<400> 73

atgaagatag gtatctttga cagtgggtgtg gggggactta ctgttctaaa ggctataaga

60

aatagataca gaaaggttga tatagtatac ctcggtgata ccgcaagggt tccctacggc

120

ataaggctta aagatacgat aatcagatac tcccttgagt gtgcgggctt tttaaaggat

180

aagggtgttg atataatcgt cgttgccctgc aataccgcaa gtgcttacgc tcttgaacgt

240

ttaaagaaaag agataaacgt tcccgttttc ggcgttattg aaccgggggt taaagaagcc

300

ttaaaaaagt caaggaataa aaaaatagga gttataggaa ctctgcaac cgtaaaaagc

360

ggagcctacc agagaaagct tgaagagggg ggagctgatg tttttgcaaa ggcctgtccc

420

ctattcgttc cccttgcgga ggaaggcttc cttgaggggg agataacaag aaaggttgta

480

gaacactacc ttaaggagtt taaaggtaag attgatactc tgattttagg atgtacccat

540

tacccccttc ttaaaaagga gataaagaag tttttgggag acgttgaagt cgttgactct

600

tccgaagccc tttcccttc cctccataac tttataaagg acgatgggtc ctcatccctt

660

gagttatttt ttacggacct ttccccaaat ctccagtttt tgattaaatt aatactcggg 720

agggattacc cggtaaaaact tgcggagggg gtttttacac attaa 765

<210> 74

<211> 262

<212> PRT

<213> Aquifex pyrophilus amino acid sequence

<400> 74

Met Lys Ile Gly Ile Phe Asp Ser Gly Val Gly Gly Leu Thr Val Leu  
1 5 10 15

Lys Ala Ile Arg Asn Arg Tyr Arg Lys Val Asp Ile Val Tyr Leu Gly  
20 25 30

Asp Thr Ala Arg Val Pro Tyr Gly Ile Arg Ser Lys Asp Phe Thr Thr  
35 40 45

Ile Ile Arg Tyr Ser Leu Glu Cys Ala Gly Phe Leu Lys Asp Lys Gly  
50 55 60

Val Asp Ile Ile Val Val Ala Cys Asn Thr Ala Ser Ala Tyr Ala Leu  
65 70 75 80

Glu Arg Leu Lys Lys Glu Ile Asn Val Pro Val Phe Gly Val Ile Glu  
85 90 95

Pro Gly Val Lys Glu Ala Leu Lys Lys Ser Phe Thr Arg Asn Lys Lys  
100 105 110

Ile Gly Val Ile Gly Thr Pro Ala Thr Val Lys Ser Gly Ala Tyr Gln  
115 120 125

Arg Lys Leu Glu Glu Gly Gly Ala Asp Val Phe Ala Lys Ala Cys Pro  
130 135 140

Leu Phe Val Pro Leu Ala Glu Glu Gly Leu Leu Glu Gly Glu Ile Thr  
145 150 155 160

Arg Lys Val Val Glu His Tyr Phe Thr Leu Lys Glu Phe Lys Gly Lys  
165 170 175

Ile Asp Thr Leu Ile Leu Gly Cys Thr His Tyr Pro Leu Leu Lys Lys

180

185

190

Glu Ile Lys Lys Phe Leu Gly Asp Val Glu Val Val Asp Ser Ser Glu  
 195 200 205

Ala Leu Ser Leu Ser Leu His Asn Phe Ile Lys Asp Asp Gly Ser Ser  
 210 215 220

Ser Leu Glu Leu Phe Thr Phe Phe Thr Asp Leu Ser Pro Asn Leu Gln  
 225 230 235 240

Phe Leu Ile Lys Leu Ile Leu Gly Arg Asp Tyr Pro Val Lys Leu Ala  
 245 250 255

Glu Gly Val Phe Thr His  
 260

<210> 75  
 <211> 19  
 <212> DNA  
 <213> Homo sapiens

<400> 75  
 tgatgcaaca aatggacga 19

<210> 76  
 <211> 18  
 <212> DNA  
 <213> Homo sapiens

<400> 76  
 ttacaatttg agccattc 18